

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/643,434A
Source: IFw16
Date Processed by STIC: 8/15/05

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IFW16

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/643,434A

DATE: 08/15/2005

TIME: 08:23:48

Input Set : A:\00786.366003.seqlist.txt
 Output Set: N:\CRF4\08152005\J643434A.raw

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3 <110> APPLICANT: Sheen, Jen
4     Kovtun, Yelena
5     Chiu, Wan-Ling
7 <120> TITLE OF INVENTION: Transgenic Plants Expressing a MAPKKK Protein Kinase Domain
9 <130> FILE REFERENCE: 00786/366003
11 <140> CURRENT APPLICATION NUMBER: 10/643,434A
C--> 12 <141> CURRENT FILING DATE: 2003-09-19
14 <150> PRIOR APPLICATION NUMBER: 09/371,338
15 <151> PRIOR FILING DATE: 1999-08-10
17 <150> PRIOR APPLICATION NUMBER: 60/095,938
18 <151> PRIOR FILING DATE: 1998-08-10
20 <160> NUMBER OF SEQ ID NOS: 24
22 <170> SOFTWARE: PatentIn version 3.3
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25 <211> LENGTH: 21
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27 <213> ORGANISM: Artificial Sequence
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53 <220> FEATURE:
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61 <211> LENGTH: 29
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63 <213> ORGANISM: Artificial Sequence
65 <220> FEATURE:
66 <223> OTHER INFORMATION: Oligonucleotide Primer

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99 <213> ORGANISM: Arabidopsis thaliana
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108 20 25 30
111 Thr Ser Cys Ile Arg Lys Ser Lys Ile Phe Ile Lys Pro Ser Phe Ser
112 35 40 45
115 Pro Pro Pro Pro Ala Asn Thr Val Asp Met Ala Pro Pro Ile Ser Trp
116 50 55 60
119 Arg Lys Gly Gln Leu Ile Gly Arg Gly Ala Phe Gly Thr Val Tyr Met
120 65 70 75 80
123 Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala Val Lys Gln Val Leu
124 85 90 95
127 Ile Ala Ala Asn Phe Ala Ser Lys Glu Lys Thr Gln Ala His Ile Gln
128 100 105 110
131 Glu Leu Glu Glu Val Lys Leu Leu Lys Asn Leu Ser His Pro Asn
132 115 120 125
135 Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Asp Asp Thr Leu Asn Ile
136 130 135 140
139 Leu Leu Glu Phe Val Pro Gly Gly Ser Ile Ser Ser Leu Leu Glu Lys
140 145 150 155 160
143 Phe Gly Pro Phe Pro Glu Ser Val Val Arg Thr Tyr Thr Arg Gln Leu
144 165 170 175
147 Leu Leu Gly Leu Glu Tyr Leu His Asn His Ala Ile Met His Arg Asp
148 180 185 190
151 Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys Gly Cys Ile Lys Leu
152 195 200 205

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155 Ala Asp Phe Gly Ala Ser Lys Gln Val Ala Glu Leu Ala Thr Met Thr
 156 210 215 220
 159 Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp Met Ala Pro Glu Val
 160 225 230 235 240
 163 Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp Ile Trp Ser Val Gly
 164 245 250 255
 167 Cys Thr Val Ile Glu Met Val Thr Gly Lys Ala Pro Trp Ser Gln Gln
 168 260 265 270
 171 Tyr Lys Glu Val Ala Ala Ile Phe Phe Ile Gly Thr Thr Lys Ser His
 172 275 280 285
 175 Pro Pro Ile Pro Asp Thr Leu Ser Ser Asp Ala Lys Asp Phe Leu Leu
 176 290 295 300
 179 Lys Cys Leu Gln Glu Val Pro Asn Leu Arg Pro Thr Ala Ser Glu Leu
 180 305 310 315 320
 183 Leu Lys His Pro Phe Val Met Gly Lys His Lys Glu Ser Ala Ser Thr
 184 325 330 335
 187 Asp Leu Gly Ser Val Leu Asn Asn Leu Ser Thr Pro Leu Pro Leu Gln
 188 340 345 350
 191 Ile Asn Asn Thr Lys Ser Thr Pro Asp Ser Thr Cys Asp Asp Val Gly
 192 355 360 365
 195 Asp Met Cys Asn Phe Gly Ser Leu Asn Tyr Ser Leu Val Asp Pro Val
 196 370 375 380
 199 Lys Ser Ile Gln Asn Lys Asn Leu Trp Gln Gln Asn Asp Asn Gly Gly
 200 385 390 395 400
 203 Asp Glu Asp Asp Met Cys Leu Ile Asp Asp Glu Asn Phe Leu Thr Phe
 204 405 410 415
 207 Asp Gly Glu Met Ser Ser Thr Leu Glu Lys Asp Cys His Leu Lys Lys
 208 420 425 430
 211 Ser Cys Asp Asp Ile Ser Asp Met Ser Ile Ala Leu Lys Ser Lys Phe
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 215 Asp Glu Ser Pro Gly Asn Gly Glu Lys Glu Ser Thr Met Ser Met Glu
 216 450 455 460
 219 Cys Asp Gln Pro Ser Tyr Ser Glu Asp Asp Glu Leu Thr Glu Ser
 220 465 470 475 480
 223 Lys Ile Lys Ala Phe Leu Asp Glu Lys Ala Ala Asp Leu Lys Lys Leu
 224 485 490 495
 227 Gln Thr Pro Leu Tyr Glu Glu Phe Tyr Asn Ser Leu Ile Thr Phe Ser
 228 500 505 510
 231 Pro Ser Cys Met Glu Ser Asn Leu Ser Asn Ser Lys Arg Glu Asp Thr
 232 515 520 525
 235 Ala Arg Gly Phe Leu Lys Leu Pro Pro Lys Ser Arg Ser Pro Ser Arg
 236 530 535 540
 239 Gly Pro Leu Gly Gly Ser Pro Ser Arg Ala Thr Asp Ala Thr Ser Cys
 240 545 550 555 560
 243 Ser Lys Ser Pro Gly Ser Gly Ser Arg Glu Leu Asn Ile Asn Asn
 244 565 570 575
 247 Gly Gly Asp Glu Ala Ser Gln Asp Gly Val Ser Ala Arg Val Thr Asp
 248 580 585 590
 251 Trp Arg Gly Leu Val Val Asp Thr Lys Gln Glu Leu Ser Gln Cys Val

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255	Ala Leu Ser Glu Ile Glu Lys Lys Trp Lys Glu Glu Leu Asp Gln Glu			
256	610	615	620	
259	Leu Glu Arg Lys Arg Gln Glu Ile Met Arg Gln Ala Gly Leu Gly Ser			
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279	ccagcctccg tttcccggtg ttctcgccga taagatcacc tcttgcatcc gcaaattcgaa	120		
281	gatttttatac aaaccctcct tctcgccctt ccctctgtct aacactgttag acatggcacc	180		
283	tccgatttcg tggagggaaag gtcagttaat tggtcgccgc gcgttggta cgggttatcat	240		
285	gggtatgaat ctgtactccg gggagcttct cggcgtaaaa cagggttctga ttgcagccaa	300		
287	ttttgcttcc aaggaaaaaga ctcaggctca tattcaggag cttgaagaag aagttaaagct	360		
289	tcttaaaaat ctctccccatc ctaatatagt tagatatttgc ggtacagtga gggaaagatga	420		
291	taccctgaat atccttctcg agttttttccg cgggtggatcg atatcatcgc tcttggagaa	480		
293	atttggacct tttcctgaat cagttgtccg gacatacaca aggcaactgc ttttagggtt	540		
295	ggagttacctg cacaatcatg caattatgcg cagagacatt aagggggcta atatccttgt	600		
297	ggataataaaa ggatgcatta agcttgctga ttttggtgc tccaaacaag tagctgagtt	660		
299	ggctacgatg actggtgcaa aatctatgaa agggacacca tattggatgg ctccggaaagt	720		
301	tatccttcaa actggacata gcttctctgc tgacatatgg agcgtcggct gtacagttat	780		
303	tgaaatggtg actgggaagg ctccctggag tcagcgtat aaagagggtt ctgttatctt	840		
305	cttcatagga acaacaaaat cacatcctcc aatacctgtat actctcttctt ctgtatgc	900		
307	agattttctg ctcaagtgtc tgcaggaggt accaaatctg cggccaaccg catctgagct	960		
309	actaaagcat cctttgtta tggggaaaaca caaggagtct gcttctactg atcttggttc	1020		
311	tgtcctgaac aatcttagca ctccactacc gttacagata aataacacca agagcactcc	1080		
313	agattctact tgcgacgatg taggtgacat gtgtactttt ggcagttga attattcact	1140		
315	tgtagatccct gtgaaatcaa tccaaaacaa aaattttatgg caacaaaatg ataatggagg	1200		
317	tgatgaagac gatatgtgtt tgatagatga tgagaatttc ttgacatttgc acggagaaat	1260		
319	gagttctacc cttgaaaaag attgtcatct gaagaagagc tgtgtatgaca taagtgatat	1320		
321	gtccattgtt ttgaagtcca aatttgacga aagtcttgcggtt aatggagaga aagagtctac	1380		
323	aatgagcatg gaatgtgacc aaccttcata ctcagaggat gatgtgagc tgaccgagtc	1440		
325	aaaaattaaa gctttcttag atgagaaggc tgcagatcta aagaagttaac agactccctct	1500		
327	ctatgaagaaa ttctacaata gtttgcacatttctcc agttgtatgg agagtaattt	1560		
329	aagtaacagt aaaagagagg acactgctcg tggttctcg aaactgcctc caaaaagcag	1620		
331	gtcacccgagt cggggcccttc ttgggtggttc accttcaaga gcaacagacg caactagttg	1680		
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335	agtttcacag gatggtgatc cagcacgggt cacagactgg aggggcctcg ttgttgacac	1800		
337	taagcaggaa ttaagccagt gtgttgctt gtcagagata gagaagaatg ggaaggaaga	1860		
339	gcttgatcaa gaactggaaa gaaagcgaca agaaatcatg cgccaaacgag ggttgggatc	1920		
341	atccccaaaga gacagaggca tgagccgaca gagagagaag tcgaggtttt catcaccagg	1980		
343	aaaatgactt gcacaaaaaaat tctccggctt tttgattttt gattgtctaa ctgtatata	2040		
345	tatctgttaac tcttatctcg ctgtatgaa aagttagacac gaggtttggc ctgtatata	2100		

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347 gattctgaac tggttgttga aggtattaga tgtgtgtaat gtgagtgtcg ggtgc	2155
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353 <213> ORGANISM: Arabidopsis thaliana	
355 <400> SEQUENCE: 9	
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361 Gly Thr Val Tyr Met Gly Met Asn Leu Asp Ser Gly Glu Leu Leu Ala	
362 20 25 30	
365 Val Lys Gln Val Leu Ile Ala Ala Asn Phe Ala Ser Lys Glu Lys Thr	
366 35 40 45	
369 Gln Ala His Ile Gln Glu Leu Glu Glu Val Lys Leu Leu Lys Asn	
370 50 55 60	
373 Leu Ser His Pro Asn Ile Val Arg Tyr Leu Gly Thr Val Arg Glu Asp	
374 65 70 75 80	
377 Asp Thr Leu Asn Ile Leu Leu Glu Phe Val Pro Gly Gly Ser Ile Ser	
378 85 90 95	
381 Ser Leu Leu Glu Lys Phe Gly Pro Phe Pro Glu Ser Val Val Arg Thr	
382 100 105 110	
385 Tyr Thr Arg Gln Leu Leu Leu Gly Leu Glu Tyr Leu His Asn His Ala	
386 115 120 125	
389 Ile Met His Arg Asp Ile Lys Gly Ala Asn Ile Leu Val Asp Asn Lys	
390 130 135 140	
393 Gly Cys Ile Lys Leu Ala Asp Phe Gly Ala Ser Lys Gln Val Ala Glu	
394 145 150 155 160	
397 Leu Ala Thr Met Thr Gly Ala Lys Ser Met Lys Gly Thr Pro Tyr Trp	
398 165 170 175	
401 Met Ala Pro Glu Val Ile Leu Gln Thr Gly His Ser Phe Ser Ala Asp	
402 180 185 190	
405 Ile Trp Ser Val Gly Cys Thr Val Ile Glu Met Val Thr Gly Lys Ala	
406 195 200 205	
409 Pro Trp Ser Gln Gln Tyr Lys Glu Val Ala Ala Ile Phe Phe Ile Gly	
410 210 215 220	
413 Thr Thr Lys Ser His Pro Pro Ile Pro Asp Thr Leu Ser Ser Asp Ala	
414 225 230 235 240	
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418 245 250 255	
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435 ttttgcttcc aaggaaaaaga ctcaggctca tattcaggag cttgaagaag aagttaaatgt	180
437 tctaaaaat ctctcccatc ctaatatagt tagatatttgc ggtacagtga gggaaatgt	240

VERIFICATION SUMMARY

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